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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/055,475

DATE: 10/03/2002

TIME: 15:05:31

Input Set : A:\EP.txt

Output Set: N:\CRF4\10032002\J055475.raw

4 <110> APPLICANT: Fisher, Paul B.
5 Kang, Dong-Chul
6 Gopalkrishnan, Rahul V.
8 <120> TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
9 ANTIPROLIFERATIVE AGENT
11 <130> FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
13 <140> CURRENT APPLICATION NUMBER: 10/055,475
14 <141> CURRENT FILING DATE: 2002-01-22
16 <150> PRIOR APPLICATION NUMBER: PCT/US01/06960
17 <151> PRIOR FILING DATE: 2001-02-28
19 <150> PRIOR APPLICATION NUMBER: 09/515,363
20 <151> PRIOR FILING DATE: 2000-02-29
22 <160> NUMBER OF SEQ ID NOS: 17
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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27 <211> LENGTH: 3365
28 <212> TYPE: DNA
29 <213> ORGANISM: homo sapiens
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34 cagcaccatc tgcttgggag aacctctcc cttctctgag aaagaaagat gtcgaatggg 180
35 tattccacag acgagaattt ccgctatctc atctcgtgct tcagggccag ggtgaaaatg 240
36 tacatccagg tggagcctgt gctggactac ctgaccttcc tgcctgcaga ggtgaaggag 300
37 cagattcaga ggacagtcgc cacctccggg aacatgcagg cagttgaact gctgctgagc 360
38 accttgagga agggagtctg gcaccttggg tggactcggg aattcgtgga ggccctccgg 420
39 agaaccggca gccctctggc cgcccgctac atgaacctg agctcacgga cttgccctct 480
40 ccacgttttg agaacgctca tgatgaatat ctccaactgc tgaacctcct tcagccact 540
41 ctgggtggaca agcttctagt tagagacgtc ttggataagt gcatggagga ggaactgttg 600
42 acaattgaag acagaaaccg gattgctgct gcagaaaaca atggaaatga atcaggtgta 660
43 agagagctac taaaaaggat tgtgcagaaa gaaaactggt tctctgcatt tctgaatgtt 720
44 ctctgtcaaa caggaaacaa tgaactgtc caagagttaa caggctctga ttgctcagaa 780
45 agcaatgcag agattgagaa tttatcacia gttgatggc ctcaagtgga agagcaactt 840
46 ctttcaacca cagttcagcc aaatctggag aaggaggtct ggggcatgga gaataactca 900
47 tcagaatcat cttttgcaga ttcttctgta gtttcagaat cagacacaag tttggcagaa 960
48 ggaagtgtca gctgcttaga tgaaagtctt ggacataaca gcaacatggg cagtgtattca 1020
49 ggcaccatgg gaagtgattc agatgaagag aatgtggcag caagagcatc cccggagcca 1080
50 gaactccagc tcaggcctta ccaaatggaa gttgccagc cagccttgga agggaagaat 1140
51 atcatcatct gccctccctac agggagtggg aaaaccagag tggctgttta cattgccaa 1200
52 gatcaactag acaagaagaa aaaagcatct gagcctggaa aagttatagt tcttgtcaat 1260
53 aaggtactgc tagttgaaca gctcttccgc aaggagtcc aaccattttt gaagaaatgg 1320
54 tatcgtgtta ttggattaag tggtgatacc caactgaaaa tatcatttcc agaagttgtc 1380
55 aagtccgtgtg atattattat cagtacagct caaatccttg aaaactccct cttaaacttg 1440

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56 gaaaatggag aagatgctgg tgttcaattg tcagactttt ccctcattat cattgatgaa 1500
57 tgtcatcaca ccaacaaaga agcagtgtat aataacatca tgaggcatta tttgatgcag 1560
58 aagttgaaaa acaatagact caagaaagaa aacaaaccag tgattcccct tcctcagata 1620
59 ctgggactaa cagcttcacc tgggtgttga ggggccacga agcaagccaa agctgaagaa 1680
60 cacattttta aactatgtgc caatcttgat gcattttacta ttaaaactgt taaagaaaaac 1740
61 cttgatcaac tgaaaaacca aatacaggag ccatgcaaga agtttgccat tgcagatgca 1800
62 accagagaag atccatttaa agagaaactt ctagaaataa tgacaaggat tcaaacttat 1860
63 tgtcaaatga gtccaatgtc agatttttga actcaaccct atgaacaatg ggccattcaa 1920
64 atgaaaaaaa aagctgcaaa aaaaggaaat cgcaagaac gtgtttgtgc agaaccattt 1980
65 aggaagtaca atgaggccct acaaattaat gacacaattc gaatgataga tgcgtatact 2040
66 catcttgaaa ctttctataa tgaagagaaa gataagaagt ttgcagtcac agaagatgat 2100
67 agtgatgagg gtggtgatga tgagtattgt gatggtgatg aagatgagga tgatttaaag 2160
68 aaacctttga aactggatga aacagataga tttctcatga ctttattttt tgaaaacaat 2220
69 aaaatgttga aaaggctggc tgaaaaccca gaatatgaaa atgaaaagct gaccaaatta 2280
70 agaaatacca taatggagca atatactagg actgaggaat cagcacgagg aataatcttt 2340
71 acaaaaacac gacagatgtc atatgcgctt tccagtgga ttactgaaaa tgaaaaaattt 2400
72 gctgaagtag gagtcaaagc ccaccatctg attggagctg gacacagcag tgagttcaaa 2460
73 cccatgacac agaatgaaca aaaagaagtc attagtaaat ttgcactggg aaaaatcaat 2520
74 ctgcttatcg ctaccacagt ggcagaagaa ggtctggata ttaaagaatg taacattggt 2580
75 atccgttatg gtctcgtcac caatgaaata gccatggtcc aggcccggtg tcgagccaga 2640
76 gctgatgaga gcacctacgt cctggttget cacagtgggt caggagttaa cgaacatgag 2700
77 acagttaatg atttccgaga gaagatgatg tataaagcta tacattgtgt tcaaatatg 2760
78 aaaccagagg agtatgtcca taagattttg gaattacaga tgcaaagtat aatggaaaag 2820
79 aaaatgaaaa ccaagagaaa tattgccaag cattacaaga ataaccatc actaataact 2880
80 ttcttttgca aaaactgcag tgtgctagcc tgttctgggg aagatatcca tgtaattgag 2940
81 aaaatgcac acgtcaatat gacccagaa ttcaaggaac ttacattgt aagagaaaac 3000
82 aaagcactgc aaaagaagtg tgccgactat caaataaatg gtgaaatcat ctgcaaatgt 3060
83 ggccaggctt ggggaacaat gatggtgcac aaaggcttag atttgccttg tctcaaaata 3120
84 aggaattttg tagtggtttt caaaaataa tcaacaaaga aacaatacaa aaagtgggta 3180
85 gaattaccta tcacatttcc caatcttgac tattcagaat gctgtttatt tagtgatgag 3240
86 gattagcact tgattgaaga ttcttttaaa atactatcag ttaaacattt aatatgatta 3300
87 tgattaatgt attcattatg ctacagaact gacataagaa tcaataaaat gattgtttta 3360
88 ctctg

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90 <210> SEQ ID NO: 2

91 <211> LENGTH: 1025

92 <212> TYPE: PRT

93 <213> ORGANISM: homo sapiens

95 <400> SEQUENCE: 2

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96 Met Ser Asn Gly Tyr Ser Thr Asp Glu Asn Phe Arg Tyr Leu Ile Ser
97 1 5 10 15
98 Cys Phe Arg Ala Arg Val Lys Met Tyr Ile Gln Val Glu Pro Val Leu
99 20 25 30
100 Asp Tyr Leu Thr Phe Leu Pro Ala Glu Val Lys Glu Gln Ile Gln Arg
101 35 40 45
102 Thr Val Ala Thr Ser Gly Asn Met Gln Ala Val Glu Leu Leu Leu Ser
103 50 55 60
104 Thr Leu Glu Lys Gly Val Trp His Leu Gly Trp Thr Arg Glu Phe Val
105 65 70 75 80
106 Glu Ala Leu Arg Arg Thr Gly Ser Pro Leu Ala Ala Arg Tyr Met Asn

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107				85				90				95	
108	Pro	Glu	Leu	Thr	Asp	Leu	Pro	Ser	Pro	Ser	Phe	Glu	Asn
109				100				105				110	Ala
110	Glu	Tyr	Leu	Gln	Leu	Leu	Asn	Leu	Leu	Gln	Pro	Thr	Leu
111			115				120					125	Val
112	Leu	Leu	Val	Arg	Asp	Val	Leu	Asp	Lys	Cys	Met	Glu	Glu
113		130					135				140		Leu
114	Thr	Ile	Glu	Asp	Arg	Asn	Arg	Ile	Ala	Ala	Ala	Glu	Asn
115	145				150				155				160
116	Glu	Ser	Gly	Val	Arg	Glu	Leu	Leu	Lys	Arg	Ile	Val	Gln
117				165					170				175
118	Trp	Phe	Ser	Ala	Phe	Leu	Asn	Val	Leu	Arg	Gln	Thr	Gly
119				180					185				190
120	Leu	Val	Gln	Glu	Leu	Thr	Gly	Ser	Asp	Cys	Ser	Glu	Ser
121			195					200				205	Asn
122	Ile	Glu	Asn	Leu	Ser	Gln	Val	Asp	Gly	Pro	Gln	Val	Glu
123		210					215				220		Gln
124	Leu	Ser	Thr	Thr	Val	Gln	Pro	Asn	Leu	Glu	Lys	Glu	Val
125	225				230				235				240
126	Glu	Asn	Asn	Ser	Ser	Glu	Ser	Ser	Phe	Ala	Asp	Ser	Ser
127				245					250				255
128	Glu	Ser	Asp	Thr	Ser	Leu	Ala	Glu	Gly	Ser	Val	Ser	Cys
129			260					265					270
130	Ser	Leu	Gly	His	Asn	Ser	Asn	Met	Gly	Ser	Asp	Ser	Gly
131			275					280				285	Thr
132	Ser	Asp	Ser	Asp	Glu	Glu	Asn	Val	Ala	Ala	Arg	Ala	Ser
133		290					295				300		Pro
134	Glu	Leu	Gln	Leu	Arg	Pro	Tyr	Gln	Met	Glu	Val	Ala	Gln
135	305				310					315			320
136	Glu	Gly	Lys	Asn	Ile	Ile	Ile	Cys	Leu	Pro	Thr	Gly	Ser
137				325					330				335
138	Arg	Val	Ala	Val	Tyr	Ile	Ala	Lys	Asp	His	Leu	Asp	Lys
139			340					345					350
140	Ala	Ser	Glu	Pro	Gly	Lys	Val	Ile	Val	Leu	Val	Asn	Lys
141			355					360				365	Val
142	Val	Glu	Gln	Leu	Phe	Arg	Lys	Glu	Phe	Gln	Pro	Phe	Leu
143		370					375			380			Lys
144	Tyr	Arg	Val	Ile	Gly	Leu	Ser	Gly	Asp	Thr	Gln	Leu	Lys
145	385				390				395				400
146	Pro	Glu	Val	Val	Lys	Ser	Cys	Asp	Ile	Ile	Ile	Ser	Thr
147				405					410				415
148	Leu	Glu	Asn	Ser	Leu	Leu	Asn	Leu	Glu	Asn	Gly	Glu	Asp
149			420					425					430
150	Gln	Leu	Ser	Asp	Phe	Ser	Leu	Ile	Ile	Ile	Asp	Glu	Cys
151			435					440				445	His
152	Asn	Lys	Glu	Ala	Val	Tyr	Asn	Asn	Ile	Met	Arg	His	Tyr
153		450					455				460		Leu
154	Lys	Leu	Lys	Asn	Asn	Arg	Leu	Lys	Lys	Glu	Asn	Lys	Pro
155	465				470				475				480

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156 Leu Pro Gln Ile Leu Gly Leu Thr Ala Ser Pro Gly Val Gly Gly Ala
157          485          490          495
158 Thr Lys Gln Ala Lys Ala Glu Glu His Ile Leu Lys Leu Cys Ala Asn
159          500          505          510
160 Leu Asp Ala Phe Thr Ile Lys Thr Val Lys Glu Asn Leu Asp Gln Leu
161          515          520          525
162 Lys Asn Gln Ile Gln Glu Pro Cys Lys Lys Phe Ala Ile Ala Asp Ala
163          530          535          540
164 Thr Arg Glu Asp Pro Phe Lys Glu Lys Leu Leu Glu Ile Met Thr Arg
165 545          550          555          560
166 Ile Gln Thr Tyr Cys Gln Met Ser Pro Met Ser Asp Phe Gly Thr Gln
167          565          570          575
168 Pro Tyr Glu Gln Trp Ala Ile Gln Met Glu Lys Lys Ala Ala Lys Lys
169          580          585          590
170 Gly Asn Arg Lys Glu Arg Val Cys Ala Glu His Leu Arg Lys Tyr Asn
171          595          600          605
172 Glu Ala Leu Gln Ile Asn Asp Thr Ile Arg Met Ile Asp Ala Tyr Thr
173          610          615          620
174 His Leu Glu Thr Phe Tyr Asn Glu Glu Lys Asp Lys Lys Phe Ala Val
175 625          630          635          640
176 Ile Glu Asp Asp Ser Asp Glu Gly Gly Asp Asp Glu Tyr Cys Asp Gly
177          645          650          655
178 Asp Glu Asp Glu Asp Asp Leu Lys Lys Pro Leu Lys Leu Asp Glu Thr
179          660          665          670
180 Asp Arg Phe Leu Met Thr Leu Phe Phe Glu Asn Asn Lys Met Leu Lys
181          675          680          685
182 Arg Leu Ala Glu Asn Pro Glu Tyr Glu Asn Glu Lys Leu Thr Lys Leu
183          690          695          700
184 Arg Asn Thr Ile Met Glu Gln Tyr Thr Arg Thr Glu Glu Ser Ala Arg
185 705          710          715          720
186 Gly Ile Ile Phe Thr Lys Thr Arg Gln Ser Ala Tyr Ala Leu Ser Gln
187          725          730          735
188 Trp Ile Thr Glu Asn Glu Lys Phe Ala Glu Val Gly Val Lys Ala His
189          740          745          750
190 His Leu Ile Gly Ala Gly His Ser Ser Glu Phe Lys Pro Met Thr Gln
191          755          760          765
192 Asn Glu Gln Lys Glu Val Ile Ser Lys Phe Arg Thr Gly Lys Ile Asn
193          770          775          780
194 Leu Leu Ile Ala Thr Thr Val Ala Glu Glu Gly Leu Asp Ile Lys Glu
195 785          790          795          800
196 Cys Asn Ile Val Ile Arg Tyr Gly Leu Val Thr Asn Glu Ile Ala Met
197          805          810          815
198 Val Gln Ala Arg Gly Arg Ala Arg Ala Asp Glu Ser Thr Tyr Val Leu
199          820          825          830
200 Val Ala His Ser Gly Ser Gly Val Ile Glu His Glu Thr Val Asn Asp
201          835          840          845
202 Phe Arg Glu Lys Met Met Tyr Lys Ala Ile His Cys Val Gln Asn Met
203          850          855          860
204 Lys Pro Glu Glu Tyr Ala His Lys Ile Leu Glu Leu Gln Met Gln Ser

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205 865                870                875                880
206 Ile Met Glu Lys Lys Met Lys Thr Lys Arg Asn Ile Ala Lys His Tyr
207                885                890                895
208 Lys Asn Asn Pro Ser Leu Ile Thr Phe Leu Cys Lys Asn Cys Ser Val
209                900                905                910
210 Leu Ala Cys Ser Gly Glu Asp Ile His Val Ile Glu Lys Met His His
211                915                920                925
212 Val Asn Met Thr Pro Glu Phe Lys Glu Leu Tyr Ile Val Arg Glu Asn
213                930                935                940
214 Lys Ala Leu Gln Lys Lys Cys Ala Asp Tyr Gln Ile Asn Gly Glu Ile
215 945                950                955                960
216 Ile Cys Lys Cys Gly Gln Ala Trp Gly Thr Met Met Val His Lys Gly
217                965                970                975
218 Leu Asp Leu Pro Cys Leu Lys Ile Arg Asn Phe Val Val Val Phe Lys
219                980                985                990
220 Asn Asn Ser Thr Lys Lys Gln Tyr Lys Lys Trp Val Glu Leu Pro Ile
221                995                1000                1005
222 Thr Phe Pro Asn Leu Asp Tyr Ser Glu Cys Cys Leu Phe Ser Asp Glu
223 1010                1015                1020
224 Asp
225 1025

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227 <210> SEQ ID NO: 3

228 <211> LENGTH: 1036

229 <212> TYPE: DNA

230 <213> ORGANISM: homo sapiens

232 <220> FEATURE:

233 <221> NAME/KEY: misc_feature

234 <222> LOCATION: 551

235 <223> OTHER INFORMATION: n = A,T,C or G

237 <400> SEQUENCE: 3

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238 gcacattttg gcctacaaag gaccttattg ttaaggcaga acctgctggg aaaacaaaat 60
239 atccgccgga ggagctttgt agagcggttg tcttggtgtc agagagaatt cgctttcctt 120
240 ttctgtttcc cgcggtgtcc ttaaccaaag gcctcctctc ttcacccgcc ccgacaaaaa 180
241 ggtggcgtct ccctgaggaa actccctccc cgccaggcag attacgttta caaagtcctg 240
242 agaagagaat cgaaacagaa accaaagtca ggcaaactct gtaagaactg cctgacagaa 300
243 agctggactc aaagctccta cccgagtgtg cagcaggatc gccccggtcc gggacccag 360
244 gcgcacaccg cagagtccaa agtgccgcgc ctgccggccg cactgcctg ccgcggcccc 420
245 gcgcgccgcc ccgtgccca cctgccgcc tgcccacctg occaggtgcg agtgcagccc 480
246 cgcgcgccgg cctgagagcc ctgtggacaa cctcgtcatt gtcaggcaca gagcggtaga 540
W--> 247 ccctgcttct ntaagtgggc agcggacagc ggcacgcaca tttcacctgt cccgcagaca 600
248 acagcaccat ctgcttgga gaacctctc ccttctctga gaaagaaaga tgtcgatgg 660
249 gtattccaca gacgagaatt tccgtatct catctcgtgc ttcagggccg gggtgaaaat 720
250 gtacatccag gtggagcctg tgcctgacta cctgacctt ctgcctgcag aggtgaagga 780
251 gcagattcag aggacagtcg ccacctccg gaacatgcag gcagttgaac tgctgctgag 840
252 caccttgag aagggagtct ggcacctgg ttggactcgg gaattcgtgg aggccctccg 900
253 gagaaccggc agccctctgg ccgccgcta catgaacct gagctcacgg acttgccctc 960
254 tccatcgttt gagaacgctc atgatgaata tctccaactg ctgaacctcc ttcagccacc 1020
255 tctggtggac aagctt
258 <210> SEQ ID NO: 4 1036

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/03/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 551

VERIFICATION SUMMARY

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Input Set : A:\EP.txt

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L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:540